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(Amended) **Figures 2A-2C. Determination of *mda*-7 transcription by nuclear run-on, *mda*-7 mRNA by Northern blotting and RT-PCR and a comparison of the AU-rich sequences found in the 3'-UTR of several mRNAs.** (Figure 2A) Nuclear run-on assays using nuclei isolated from Control or 24 h after treatment with IFN-β, MEZ or IFN-β + MEZ, the same concentrations as indicated in Fig. 1. GAPDH was used as an internal control. In vitro transcription assays were performed as previously described (*Jiang et al.*, 1993). (Figure 2B) *Mda*-7 message expression detected by Northern blotting and RT-PCR followed by Southern blotting. Total RNA from control (Figure 2C) HO-1 cells and cells treated with IFN-β (I), MEZ (M) or IFN-β +MEZ (I+M) were analyzed by Northern blotting or RT-PCR/Southern using radiolabeled *mda*-7 cDNA as a probe as previously described (Jiang *et al.*, 1993, 1995a; Kang *et al.*, 1998a). GAPDH was used as an internal loading control. (C) Several cytokine genes and proto-oncogenes that contain the AUUUA consensus sequence in their 3'-UTRs. Abbreviations: Hu = human; *mda*-7 = melanoma differentiation associated gene-7 (Jiang *et al.*, 1995a); α-IFN = alpha interferon (Goeddel *et al.*, 1981); GM-CSF = granulocyte-monocyte colony stimulating factor (Wong *et al.*, 1985); TNF = tumor necrosis factor (Nedwin *et al.*, 1985); cFos = fos proto-oncogene (van Straaten *et al.*, 1983). (SEQ ID NOS:9-13).

Please amend the paragraph on page 57, line 25 through page 58, line 5. A clean version of the amended paragraph follows:

A2

(Amended) ***Isolation and cloning of the mda-7 promoter.*** A human placental genomic 1 library (Stratagene) was screened using the *mda*-7 cDNA (18) labeled by random priming (Life Technologies, Inc.)

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using α-^{32}P[dCTP]. Three l phage clones were identified and isolated to homogeneity. An anti-sense primer, 5'-CGTCCCAGCCGTGGAAGTCAT-3' (SEQ ID NO:2) corresponding to the region 40-50 bp from the 5' terminal end of the *mda*-7 cDNA was used with the T3 or T7 primer in a polymerase chain reaction to amplify the region upstream of the *mda*-7 cDNA from the three l phage clones. The proof reading polymerase, Tth polymerase (Clonetech) was employed for this purpose. One of the l phage clones yielded a 2.2 Kbp amplification product that was cloned into pBluescript and sequenced (ABI sequencing).

Please amend the paragraph on page 59, line 20 through page 60, line 12. A clean version of the amended paragraph follows:

A3

(Amended) ***Electrophoretic Mobility Shift Assay (EMSA).*** Nuclear extracts were prepared as described (25). Briefly, binding reactions were performed in 10 or 20 ml reaction mixtures containing 1-3 mg of nuclear extracts from control or differentiation inducer treated HO-1 cells. The binding buffer contained 12 mM HEPES (pH 7.9), 5 mM $MgCl_2$, 60 mM KCl, 0.6 mM EDTA, 0.5 mM dithiothreitol, 1 mg of poly (dI-dC), 10% glycerol. The region corresponding to the putative AP-1 and C/EBP binding sites present between NdeI and NheI restriction enzyme sites was PCR amplified using flanking primers, 5'-AGGCTGGATTTG GCTTGTGAC-3'(Sense)(SEQ ID NO:3) and 5'-CTGTTTAATCCAGCACTTCCC-3' (Antisense) (SEQ ID NO:4). The PCR product was column purified (Qiagen), end labeled with γ-^{32}P [ATP] and 1500 cpm of double stranded DNA were used per binding reaction. Binding reactions were performed at RT for 30 min. Reactions were then loaded onto a 4% polyacrylamide gel and electrophoresed at 4^0 C at 100 V in 0.25X Tris-borate-EDTA as described (26,27). Competition and supershift reactions were identical to those described above, except a 10-100 fold excess of

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